Sequence:

Run on:

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Maximum Match 100%
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                                             - nucleic search, using sw model
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U25128 Human PTH2 G26909 human STS S U55836 Rettus norv U47129 Human parat AC019822 Homo sapi AC019185 Homo sapi AF132082 Danio rer AF132084 Danio rer I17764 Sequence 1 I17765 Sequence 2 M74445 Opossum par L19475 Rat parathy

G26909 RNU55836 HSPTHR05 AC010822 AC019185 AF132084

93 17 17 13 13 13 13

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HSU25128

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DB

Description

SUMMARIES

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AF132083 Mus muscu
AC012362 Homo sapi
U94326 Meleagris g
AF100644 Rana ridi
AF132081 Ictalurus
AF025411 Oryctolag
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U13989 Human secre
U20178 Human secre
128734 Sequence 1
U49434 Sus scrofa
117766 Sequence 3
M77184 Rat parathy
X78936 M.musculus
AF167095 Canis fam
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                                                                 X68596 H.sapiens m
U17418 Human parat
AF132085 Danio rer
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L13288 Human vasoa
E04128 cDNA encodi.
                                     L04308 Human parat
U18315 Sus scrofa
I17767 Sequence 4
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U31991 Meleagris g
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Submitted (17-APR-1995) Tom I. Bonner, Lab of Cell Biology, NIMH,
Bldg. 36, Room 3A-17, Bethesda, MD 20892-4090, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function-"stimulates cAMP production in response to parathyroid hormone but not parathyroid hormone-related peptide"
                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1995
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Human PTH2 parathyroid hormone receptor mRNA, complete cds.
U25128.1 GI:887966
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/db_xref_"taxon:9606"
/tissue_type-"cerebral cortex and hippocampus"
/143. .1795
/noter"G protein-coupled receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"PTH2 parathyroid hormone receptor'
/protein_id~"AAC50157.1"
         RATPATHYR
MMPHRPR
AF167095
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Bonner, T.I.
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TITLE
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VERSION

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CNPNGTWDFWHSLMTAAQLGGEGGNCPFEWDGLICWRGTGNGTISGCGFFRLLYWTYTGTSISGSLA
VALLIGYFRRLHCTRYNIHWHLFVSFMLRATSIFVKDRTVHAHIGVKELESGLIMODD
PQNSIEATSVDKSOYIGCK LAVVWFIYFLTRINY WHLUMGLYLHNILFVAFFSDTKYL
WGFILLGWGFPAAFVAMAVARATLADARGWELSAGDIKHIYOPAILAAGLMFILFL
NTWRYLART WBTHAAGHDYRKQY RKLAKSTLVLULVEGWHYYOPAILAAGLMFILFL
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FHTTTTHYSTSCSQOYAASTRWYLISGRAAKTASRQPOSHITLRGYWWSNSEQDCLPHS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2641)
Myers, R.M.
                                       1988
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for
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA
Fex: 4157259687
                                                                                                                                                                                       DNA STS sequence tagged site.
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ndels 2; Gaps agggtccctgctc 69                 AGGGTCCCTGCTTC 122	tggggttggc 129           TGGGGTTGCC 182	catcacta 189               CATTACTA 242	acag 249        CAG 302	gc 309     3C 362	a 369   A 422	429	89	o 0	o 0	6 C	6 R	6 8	o 0	5 6	2 2	6 G
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34 Similarity 99.0%; Pred. No. U; 1975; Conservative 0; Mismatches 18; I gggcagccaagttggcatattggaagcttttccgggctctggagg	ttcctacagccgttccgggcatggctggctgggggggtcgctccacgtc 	taatgeteggeagetgeetetggeeagageecagetggattetgatggeae 	tagaggagcagattgtccttgtgctgaaagcgaaagtacaatgtgaactcaacatcacag 	ctcaactccaggaggagaggtaattgtttcctgaatgggatggat	ccagaggaacaqtggggaaalatcggctgttccatgcctccttatatttatgacttc 	accataaagggttgctttccgacactgtaaccccaatggaacatgggttttatgcaca 	gcttaaataaaacatgggccaattattcagactgccttcgcttctgcagccagatatca 	gcataggaaagcaagaattctgtgaacgcctctatgtaatgtataccgttggctactcca 	<pre>tctcttttggttccttggctgtggctattctcatcattggttacttcagacgattgcatt                                    </pre>	gcactaggaactatatccacatgcacttatttgtgtctttcatgctgagagctacaagca 	LCtttgtcaaagacagagtagtccatgctcacataggagtaaaggagctggagtcctaa 	taatgcaggatgacccacaaaattccattgaggcaacttctgtggacaaatcacaatata 	togggtgcaagattgctgttgtgatgtttatttacttcctggctacaaattatttgtga 	<pre>Lectggtggaaggtetetacetgcataateteatetttgtggetttettteggacacea                                  </pre>	<pre>aatacctgtggggcttcatcttgataggctgggggtttccagcagcatttgttgcagcat {                                    </pre>	gggctgtggcacgagcaactctggctgatgcgaggtgctgggaacttagtgctggagaca 
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ROD 19-OCT-1996 receptor PTH2 mRNA, complete

RNU55836 1977 bp mRNA Rattus norvegicus parathyroid hormone cds.

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SE 2 (bases 1 to 1977)

RS Bonner, T. I. and Usdin, T. B.

S Direct Submission

NAL Submitted (19-APR-1996) Tom I. Bonner, Lab of Cell Biology, NIMH,

Bldg 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA

LOCATION/Qualifiers

Source /Organism="Rattus norvegicus"

/ Organism="Rattus norvegicu
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                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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Pred. No. 0;
5; Mismatches 299; Indels
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Usdin,T.B., Bonner,T.I., Harta,G. and Mezey,E.
Distribution of parathyroid hormone-2 receptor
                                                                                                                                                                                                                                                                          ribonucleic acid in rat
Endocrinology 137 (10), 4285-4297 (1996)
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                                                                        Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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llarity 81.5%;
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Best Local Similarity
Matches 1397; Conserv
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1142 1082 catgacacaaggaagcaatacaggaaactggccaaatcgacactggtcctggtcctagtc 1202 1262 1322 1442 1261 1441 1561 1022 1381 1501 1321 1621 1561 1681 722 782 842 664 724 784 844 904 atctactgctactgcaatggagaggttcaggcagaggtgaagagtggagtcggtgg ggagacatcaagtggatttatcaagcaccgatcttagcagctattgggctgaattttatt 1442 GTCTATTGCTACTGCAACGGAGGGAGGGTGAGGTGAAGAAGAAGACCTGGACTCGTTGG ctcaccaccgtgacgcacagcaccagcagcagtcacagttgcggc-agcacacgcatg -GCTTTCTGCAGCCT gcagcatgggctgtggcacgagcaactctggctgatgcgaggtgctgggaacttagtgct CTCACCACTGTCACACACACACCAGCAGCCAGTCACAGATGGGACCAAGCACACGCCTG

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Length 1980; Indels

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AC010822 159700 bp DNA HTG 01-APR-2000
Homo sapiens clone RP11-3M22, WORKING DRAFT SEQUENCE, 13 unordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                           aggcagagagatgatattetaatggagaagcettecaggeetatggaatetaaeeceagae 1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 620; DB 91;
Pred. No. 4.7e-167;
0; Mismatches 10;
ILMEKPSRPMESNPDTEGCQGETEDVL.
                                                                                                                                 u
                                                                                                                                 620
                                         2.4
             <1. .726
/gene="PTHR2"
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/27 . 1968
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                437
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98.2%;
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Matches 648; Conservative
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YGHDTRKQYRRLAKSTLVLUFGVHYITVRVCLHFFFGLGWBTRMHCSPGFF
FVSIIYCVGGRQABEKKMWSRWILSYDMKRTPPGSRRCGSVLTTYTHSTSSOSOY
AASTRMVLISGKAAKIASRQPDSHITLLPGYVWSNSEQDCLPHSFHEEFKEDSGRGGDD
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1980) Usdio, T.B., Gruber, C. and Bonner, T.I. Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor 5. Biol. Chem. 270 (26), 15455-15458 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1980)
Usdin,T.B., Modi.W. and Bonner,T.I.
Assignment of the human PTH2 receptor gene (PTHR2) to chromosome 2433 by fluorescence in situ hybridization
Genomics 37 (1), 140-141 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lab of Cell Biology, NIMH,
MD 20892-4090, USA
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                                                                      1681
                                                                                           1742 GAG-ACTAAAAAAGGTCATGGGCGACAGGAGAGATGATGATAGTCCAGTGGGGGGAGTCTTCCAG 1800
                                                                                                                              gcctatggaatctaacccagacactgaaggatgacaaggagaaactgaggatgttctctg 1741
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U47128.1:7. .48,727. .1968)
/gene="PTHR2"
                                                                                                                                                        1801 GCCAGTAGCATTCACCATAGACACGGAAGGATGCAAGGGAGAATC---CCACCCTATCTG 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .95,047127.1:365.
                                                                                                                                                                                                                                                                              HSPTHR05 1980 bp DNA PRI 21-OCT-1996 Human parathyroid hormone receptor (PTHR2) gene, exon 13 and partial cds.
            gagcaacaaggaagatagtgggaggcagagatgatgatattctaatggagaagccttccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map-"2q33"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="parathyroid hormone receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(U47125.1:<363. .429,U47126.1:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-JAN-1996) Tom I. Bonner,
Bldg. 36, Rm 3A17, MSC 4099, Bethesda,
Location/Qualifiers
1. .1980
                                                                                                                                                                                       .1122)
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Bonner,T.I. and Usdin,T.B.
Direct Submission
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AUTHORS
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AUTHORS
TITLE
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TITLE
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41949 AGGTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGTGGAACCTCTCCGTGGACTGGAAAA 41890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1644 aggcagagagatgatattctaatggagaagccttccaggcctatggaatctaacccagac 1703
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61167 80698: contig or 100 bp
80699 80798: gap of 100 bp
80799 103166: contig of 22368 bp in length
103167 103266: gap of 100 bp
103267 129867: contig of 26601 bp in length
12868 129967: gap of 100 bp
12968 159700: contig of 29733 bp in length.
Location/Qualifiers
1.159700
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/clone_lib="RPCI-11 Human Male BAC"
1. .1067
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Pred. No. 9.5e-167;
0; Mismatches 10;
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/note="assembly_fragment"
22244. .29636
/note="assembly_fragment"
29737 .37603
/note="assembly_fragment"
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ture 103267. .129867
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ture 129968. .159700
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1168. :5145
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/note="assembly_fragment
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Best Local Similarity 98.2%;
Matches 648; Conservative
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State 159700)

Baldwin, J., Barnana, N., Bockerly, R., Boguslawkiy, L., Boukhgälter, B.,

Baldwin, J., Barnana, N., Beckerly, R., Boguslawkiy, L., Boukhgälter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Brown, A., Castle, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M.,

Ferreirap. P. Fitzhugh, W., Forrest, C., Funce, R., Gage, D.,

Galagan, J., Gardyna, S., Grank, G., Wann, L., Karatas, A., Hein, J.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

McEwan, P., McGurk, A., McKerana, K., Macdaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R. Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Direct Submission

Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome

Rosearch, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 30, 2000 this sequence version replaced gi:6454017.

All repeats were identified using Repeatwasker:

Sanit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 157000; agarose-fp
Insert size: 158500; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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Center clone name: 3_k_22

Center clone name: 3_k_22

Sequencing vector: M13; M77815; 100% of reads

Chanistry: Dye-terminator B19 Dye; 100% of reads

Assembly program: Phrap; version 0 960731

Consensus quality: 145599 bases at least Q40

Consensus quality: 151691 bases at least Q20

Consensus quality: 154613 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37604 37703: gap of 100 bp 37704 47116: contig of 9413 bp in length 47117 47216: gap of 100 bp 100 bp 61066: contig of 13850 bp in length 61067 61166: gap of 100 bp
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1068 1167: gap of 100 bp
1168 5145: contig of 3978 bp in length
5246 11674: contig of 6429 bp in length
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22143: contig of 6025 bp in length
22243: gap of 100 bp
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37603: contig of 7867 bp in length
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                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-3M22
Unpublished
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/note="assembly_name:Contig15
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-299P7"
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Homo sapiens chromosome 2 clone RP11-299P7, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173316)
                                                                                                                                        41530 TCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGCTTGGCTGATACTCCTATGCTTGA 41471
                                                                                                                                                                                                            41470 GTTCAAAGGCTGAAAATTCAGTTAAAGGTGTTACTTAATAATAATTAGTTTTTAGGCTCCATGAA 41411
                                                                                                                                                                                                                                                                 41650 AGGCAGGGAGATGATATTCTAATGGAGAAGCCTTCCAGGCCTATGGAATCTAACCCAGAC 41591
                                                                                                                                                                                                                                               1884 ttggctcctgtaaatactaacgacatgaaaatgcaagtgtcaatggagtagtttattacc 1943
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mon 63108, USA
On Jul 15, 2000 this sequence version replaced gi:8980958.
                                    ACTGAAGGATGCCAAGGAGAAACTGAGGATGTTCTCTGAATGGACATTTGTGGCTGACTT
                                                                                                        gcacaaaggctgaaaattcagttaaggtgttacttaataatagtttttaggctccatgaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; $
Sequencing vector: plasmid; $
Chemistry: Dye-terminator Big Dye; $ of reads
Chemistry: Dye-terminator Big Dye; $ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170008 bases at least Q40
Consensus quality: 170008 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 172516; sum-of-contigs
Quality coverage: 5.71 in Q20 bases; agarose-fp
Quality coverage: 5.71 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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Db 154807 GGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAGTGCTCACCACCGTGAGGCACAGCA 154866
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                                                                                                                                     gap of unknown length
contig of 25462 bp in length
gap of unknown length
contig of 47606 bp in length
gap of unknown length
gap of unknown length
contig of 53649 bp in length.
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                                                                                  of 12983 bp in length
unknown length
of 15275 bp in length
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                                 unknown length
of 9986 bp in length
unknown length
unknown length
               of 4029 bp in
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/note-"assembly_name:Contig16"
31025. 46299
/note-"assembly_name:Contig17"
46400. 71861
71962. 119567
/note-"assembly_name:Contig18"
71968. 173316
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/note="assembly_name:Contigl3"
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 2429)
Rubin, D.A., Hellman, P., Zon, L.I., Lobb, C.J., Bergwitz, C. and
                                              ACTCAGAGGACTGCCTGCCACACTCTTTCCACGAGGAG-ACCAAGGAAGATAGTGGG 155045
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Submitted (01-MAR-1999) Endocrine Unit, Wellman 5, Massachusetts
General Hospital, Fruit Street, Boston, MA 02114, USA
Location/Qualifiers
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Rubin,D.A., Hellman,P., Zon,L.I., Lobb,C.J., Bergwitz,C. and
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/db_xref="GI:5805257"
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/db_xref="taxon:7955"
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Danio rerio parathyroid hormone
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Actinopterygil; Neopterygil; Teleostei; Euteleostei; Ostariophysi;
Oypriniformes; Cyprinidae; Rasborinae; Danio.

(bases 1 to 2129)
Rubin, D.A. and Juppner, H.
Robrafish express the common parathyroid hormone/parathyroid
hormone-related peptide receptor (PTHIR) and a novel receptor
(PTH3R) that is preferentially activated by mammalian and fugufish
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Rubin,DA. and Jueppner,H.
Direct Submission
Submitted (26-PEB-1999) Endocrine Unit, Wellman 5, Massachusetts
General Hospital, Fruit Street, Boston, MA 02114, USA
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hormone receptor PTH1R mRNA, complete
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J. Biol. Chem. 274 (40), 28185-28190 (1999)
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TITLE
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Pred. No. 1.3e-128;
0; Mismatches 481;
/dev_stage="adult"
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Db 451 AGTGCCGGCAAGGTGGCGGTGCCTGCCCGACTACTTCTACGACTTCAACAAA 510	Qy 377 aggagttgctttccgacactgtaaccccaatggaacatgggatttatgcacagcttaaa 436 	Oy 437 taaaacatgggccaattattcagactgccttcgctttctgcagccagatatcagcatagg 496	Oy 497 aaagcaagaattctgtgaacgcctctatgtaatgtataccgttggctactccatcttt 556   1   1   1   1   1   1   1   1   1	Qy 557 tggttccttggctgtggctattctcatcattggttacttcagacgattgcattgcactag 616	Oy 617 gaactatatccacatgcacttatttgtgtctttcatgctgagagctacaagcatctttgt 676	Qy 677 caaagacagagtagtccatgctcacataggagtaaaggagctggagtcctaataatgca 736	Qy 737 ggatgacccacaaaattccattgaggcaacttctgtggacaaatcacaatatcgggtg 796	Oy 797 caagattgctgttgtgatgtttatttacttcctggctacaaattattggatcctggt 856   1   1   1   1   1   1   1   1   1	Oy 857 ggaaggtctctacctgcataatctcatctttgtggctttcttt	Qy 917 gtggggetteatettgataggetgggggtttecageagtttgttgeageattggetgt 976	Oy 977 ggcacgagcaactctggctgatgcgaggtgctgggaacttagtgctggagacatcaagtg 1036	Oy 1037 gatttatcaagcaccgatcttagcagctattgggctgaattttattctgtttctgaatac 1096	Oy 1097 ggttagagttctagctaccaaaatctgggagaccaatgcagttgggcatgacacaaggaa 1156	Oy 1157 gcaatacaggaaactggccaaatcgacactggtcctggtcctagtctttggagtgcatta 1216	Oy 1217 catcgfgftcgfgfgctgcctcactccttcactgggctcgggfgggagatccgcat 1273	OY 1274 geactgtgagctcttctcaactcctttcagggtttctttgtgtctatcatctactgcta 1333   1402 GCACTATGAATGCTCTTCAATTCCAGGGATTTTTCGTTGCTATATATA	<ul> <li>QY 1334 ctgcaatggagaggttcaggcagaggtgaagatgtggagtcgtggtggaatctctccgt 1393</li> <li>DE 1462 CTGCAATGGAGGTACAAGGCAGATCAAGAAGTCATGGAGCCGATGGACCTGGCCTT 1521</li> </ul>	Oy 1394 ggactggaaaaggacaccgccatgtggcagccgcagatgcggctcagtgctca 1446
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	942 gggtttccagcagcatttgttgcagcatgggctgtgggcacgagcaactctggctgatgcg 1001	1002 aggtgctgggaacttagtgctggagacatcaagtggatttatcaagcaccgatcttagca 1061 	1062 gctattgggctgaatttattctgtttctgaatacggttagagttctagctaccaaaatc 1121 	1122 tgggagaccaatgcagttgggcatgacacaaggaagcaatacaggaaactggccaaatcg 1181   1	1182 acactggtcctggtccttggagtgcattacatcgtgttcgtgtgcctgcc	1242 tccttcactgggctcgggtgggagatccgcatgcactgtgagctcttcttcaactcc 1298 	1299 tttcagggtttctttgtgtctatcatctactgctactgcaatggagagttcaggcagag 1358 	1359 gigaagaagatgiggagicggiggaatctciccgiggactggaaaaggacaccgccatgt 1418   111111	1419 ggcagccgcagatgcggctcagtgctca 1446 	RESULT 9 117764 117764 1962 hz hwa nam 02.com 1006	ce 1 from patent US 5494806.	. dnk Gno	C, S	HILL	408 a	Query Match 22.6%; Score 452.6; DB 5; Length 1862; Best Local Similarity 63.0%; Pred. No. 6.8e-119. Matches 752; Conservative O. Mismatches 429; Indels 10. Cans	gaggagaaaggtaattgtttccctgaatgggatggactcatttgttgcccagagg 316	

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Segre, G.V., Kronenberg, H.M., Abou-Samra, A., Juppner, H., Potts, J.T.
Jr. and Schipani, E.
DNA and vectors encoding the parathyroid hormone receptor,
transformed cells, and recombinant production of PTHR proteins and
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GGACTTCAAGCGGAAGGCCCGGAGTGGCAGCAGTACCTACAGCTATGGCCCCA 1574
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Pred. No. 6.8e-119;
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                                                         DNA
IS 5494806.
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495 c 522 q
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Location/Qualifiers
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2 from patent
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63.0%;
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Bost Local Similarity 63.09
Matches 752; Conservative
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My445.1 GI:164288
G protein; parathyroid hormone receptor.
Didelphis virginiana kidney cDNA to mRNA.
Didelphis virginiana
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
1 (bases I to 1878)
Juppner, H., Abou Samra, A.-B. B., Freeman, M.W., Kong, X.F.,
Schipani, E., Richards, J., Kolakowski, L.F. Jr., Hock, J., Potts, J.T.,
Kronenberg, H.M. and Segre, G.
A G-protein linked receptor for parathyroid hormone related peptide
Science 254, 1024-1026 (1991)
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/protein_id="aaa30979.1"
/db_xxef="G1:164289"
/translation="MGAPRISALLICCSVLSSVYALVDADDVITKEEQIILLRNA
QAQCEQRIKEVIRVPELAESAKDWARSAKTKKERPAEKLYSQAEESREVSDRSRLQD
GFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHKGRAYRRCDSNGSWELVPGNNRT
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/note="also binds parathyroid hormone related peptides"
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GGAAGGCCTCTACCTTCACAGCCTCATCTTCATGGCTTTTTTTCTCTGAGAAAAAGTATCT 1041
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                                                     gtggggcttcatcttgataggctgggggtttccagcagcattgttgcagcatgggctgt
                                                                                                                                                                                         AATCAGAGTCCTGGCTACTAAACTCCGGGAGACCAATGCAGGGAGATGTGACACGAGGCA
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                                                                                                       1042 CTGGGGTTTCACATTATTTGGCTGGGGCCTCCCTGCCGTGTTTGTCGCTGTGTGGGGTGAC
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receptor mRNA, complete cds.
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114. .173
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L19475.1 GI:467316 parathyroid hormone;
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TROOTRALLANESSLVAMAIVENATBYTBYSOSILWOVMHYEMENSPOGFEVA
IIVOFONGRVQAHTSKWIKKSWIRWILALDFRRARSGSSTYSYGPWYSHTSVTNYGPRGGI
ALSLSPRLAPGAGASANGHHQLPGYVKHGSISENSLPSSGPEPGTKDDGYLNGSGLYE
WANY SECVKFLTNETREREVFDRLGMIYTVGY SISLGSLTVAVLLIGYFRRLHCTRNY
IHMHLFVSFMLRAVSIFIKDAVLYSGVSTDEIERITEEELRAFTEPPPADKAGFVGCR
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                                                                                                                                                                                                                 ä
                                                                                                           /note="also binds parathyroid hormone related peptides"
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502 c 527 g 439 t
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                                                                                                                                                                                       Length 1878;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                       Score 452.6; DB 3;
Pred. No. 6.8e-119;
); Mismatches 429;
                                                                                   PMVGEQPPPLLEEERETVM"
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63.0%;
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QGFFVAIIYCFCNGEVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGFPWYSHTSVTNV
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Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) line: chromosomal assignment of the gene in the human, mouse, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae;
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1178 GATCATACAGGTGCCCATCCTGGCAGCTATTGTGGTGAACTTTATTCTTTTTATCAATAT 1237
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Sciurognathi; Muridae;
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/organism="Rattus norvegicus"
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46 .117
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Rat parathyroid hormone/parathyroid
receptor mRNA, complete cds.
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Mammalia; Eutheria; Rodentia;
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Genomics 20 (1), 20-26 (1994)
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GPRACLSLPLSPRLPPATTNGHSQLPCHAKPGAPATETETLPVTMAVPKDDGFLNGSC
SGLDEEASGSARPPPLLQEEWETVM"
118. .1818
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                             hormone
                                                                                                           15;
                                                                                       Length 1836;
                           /product="parathyroid hormone/parathyroid
related-peptide receptor"
539 c 538 g 392 t
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Segre,G.V., Kronenberg,H.M., Abou-Samra,A., Juppner,H., Potts,J.T.
Jr. and Schipani,E.
DNA and vectors encoding the parathyroid hormone receptor,
transformed cells, and recombinant production of PTHR proteins and
aatacaggaaaactggccaaatcgacactggtcctggtcctagtctttggagtgcattaca 1218
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Sequence 3 from patent US 5494806
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parathyroid hormone receptor; parathyroid hormone-related receptor;
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Kattus norvegicus cDNA to mRNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Kong, X.-F., Schipani, E., Urena, P., Richards, J., Bonventre, J.V.,
                                                                                                                 916
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Rat parathyroid hormone receptor mRNA, complete cds.
M77184
tccacatgcacttatttgtgtctttcatgctgagagctacaagcatctttgtcaaagaca
                                                        CTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGCGCCTCACACAGAGGAGGAGGATTGC
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                                             gagtagtccatgctcacataggagtaaaggagctggagtccctaataatgcaggatgacc
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CTATALS AT 101 - "MGARIAPSLALLLCCPVLSSAYALVDADDVFTKEEQIFLLHRA
OAQCDKILKEVLHTAANIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSR
RRGRPCLLEBUNIVGWPLGAPGEVORAYPCPDIT TYDFNIKGHAYRRCDRNGSWEVYPGH
NRTWANSECHKEMTNETREREVFDRLGHTYVGS SINSLASLTVAVLILAYFRRLHCT
RNYIHMIMELSPRLANSIFVKDAVLYSGFTLDEABRITEEELHIIAQVPPPPRAAAY
VYAVWQVRYATLANTGCWDLSSGHKKWIIQVPILEASVLLHEILEINIIRVLFFFIFGMGLPAV
NAGRODTROOTRELLESTLULVPLFCVHYTVEMALLYTEVSGTLWQIQMHYBMI.FNSF
QGFFVAIIYCRCNGEVQAEIRKSWSRWTLALDFKRKRASGSSSYSYGPWVSFFINSTVN
OAGRODTROOTRELLESTLULVPLEVHYTVEMALLYTEGSSSSYSYGPWVSFFINSTVN
OAGRODTROOTRELLESTLULVPLEVHYTVEMALLYTEGSCSSYSYGPWVSFFINSTVN
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OAGRODTROOTRELLESTLULVPLEVHYTVEMALPYTEGSCSSYSYGPWVSFFINSTVN
OAGRODTROOTRELLESTLULVPTANAVPKDGFLNGSC Potts, J.T., Kronenberg, H.M. and Segre, G.V.
Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone related peptide from rat osteoblast-like cells. A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736 (1992) and 3, Expression cloing of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracelular free 444 504 564 624 reacegregererecrearecrescerarrrrassecsecrescaesecsecaeraea 736 684 ggaaaatatcggctgttccatgccctccttatatttatgacttcaaccataaaggagttg 384 aattetgigaaegectetatgiaaigitataeegitggetaetecatetettiggiteet tggctgtggctattctcatcattggttacttcagacgattgcattgcattaggaactata gagaaggtaattgtttccctgaatgggatggactcatttgttggcccagaggaacagtgg gggccaattattcagactgccttcgctttctgcagccagatatcagcataggaaagcaag 563 GGGCCAACTACAGCGAGTGCCTCAAGTTCATGACCAATGA-----GACGCGGGAACGGG Length 2065; Indels /product="parathyroid hormone receptor" 73. .1848 /codon\_start=1 /product="parathyroid hormone receptor" /protein.id="AAAA1811.1" /db\_xref="G1:206035" hormone receptor" 435 t Score 445.2; DB 12; Pred. No. 9.3e-117; ); Mismatches 423; Location/Qualifiers
1. 2065
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/cell\_line="osteosarcoma"
73. .135 SGLDEEASGSARPPLLQEEWETVM" 136. .1845

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Karperien,M., Van Dijk,T.B., Hoeijmakers,T., Cremers,F.,
Abou-Samra, B., Boonstra,J., De Laat,S.W. and Defize,L.H.K.
Expression pattern of parathyroid hormone
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Direct Submission
Submitted (21-APR-1994) M. Karperien, The Netherlands Inst. of
Developmental, Biology, Uppsalalaan 8, 3584 CT Utrecht, NETHERLANDS
Location/Qualifiers
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GYAGCRVAVTFFLYFLATNY WILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAV
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NRTWANYSECLKFWTNETREREVFDRLGMIYTVGYSMSLASLIYVAVLLILAYFREHUCT
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related peptide receptor mRNA in mouse
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Karperien, M.
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A cDNA clone (T59619) codes for a 7-transmembrane receptor (W12695) which has been identified as a human G-protein parathyroid hormone (PTH) receptor, designated HLTDG74. It was isolated from a human T cell lymphoma tissue cDNA library. The cDNA can be utilised in the prodn. Of recombinant HLTDG74 and to design probes e.g. to detect mutations in the receptor gene. Gene therapy methods can be used to treat e.g. hypocaleamla, hyperphosphatemla, hypoparathyroidism and chronic tetany by stimulating in increase in serum calcium levels. Antisense constructs can be used to inhibit the receptor e.g. for the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
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                                                                                                                                                                                                                                                                                         Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer; opossum; transgenic animal;
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                                                                                   DNA encoding vertebrate parathyroid hormone receptor - useful diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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receptor (R92275). To obtain OK-H, an opossum kidney (OK) cell cDNA library in pcDNA1 was used to transfect COS cells, and transfectants were selected for ability to bind labelled PTH. Another cDNA clone, OK-O (T15946), was also isolated in this screening; OK-H and OK-O may represent 2 separate genes or may result from a laboratory artifact. Recombinant receptors are produced in vector/host cell systems. The host cells can also be used for diagnostic measurement of PTH serum levels. Transgenic chickens that overexpress the receptor in their oviduct lay eggs of higher calcium content.
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  438 T; 0 other;
                                                           DB 20;
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  BP; 408 A; 495
                                                           22.6%;
63.0%;
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Sequence 1862
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rotal RNA was isolated from opossum kidney (OK) cells and used to prep. a cDNA library. The resultant phage libraries were used to transform E. coll conty. a larger helper plasmid pay. The cells were screened to isolate those expressing functionally intert OK cell parathyroid hormone/parathyroid hormone related protein (PTH/PTHFP) receptor proteins, performed according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying colonies capable of binding a suitable radiolabelled ligand. The clone OK-O is identical to the OK-H clone exept at the C-terminal tail as OK-O encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids. The difference is attributed to a single nucleotide deleted in the OK H sequence causing a frame shift and an earlier stop codon. It is not known whether OK-O and OK-H represent prods. Of two separate genes or are a laboratory carlifact. The clone encodes a protein which may be used in a therapeutic compsn. to inhibit activation of PTH or PTHFP and thus
ctgcaatggagaggttcaggcagaggtgaagatgtggagtcgggtggaatctctccgt 1393
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(differential) diagnosis of hypercalcaemia, and diagnosis
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reduce the level of calcium in the blood. Cpds. capable of competing with PrH or PHTPF for binding can be identified using the protein prod, and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also Q29604.11.
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                                                                                                                                                                   Length 1863;
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Pred. No. 1.7e-134;
0; Mismatches 429; Indels
                                                                                                                      Sequence 1863 BP; 411 A; 494 C; 518 G; 440 T; 0 other;
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                                            gcaatacaggaaactggccaaatcgacactggtcctggtcctagtctttggagtgcatta
                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding vertebrate parathyroid hormone receptor - useful diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
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91US-0681702
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represent 2 separate genes or may result from a laboratory artifact. Recombinant receptors are produced in vector/host cell systems. The host cells can also be used for diagnostic measurement of FTH serum levels. Transgenic chickens that overexpress the receptor in their oviduct lay eggs of higher calcium content.
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0; Mismatches 429;
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63.0%;
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Gaps

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Indels

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DB 20;

Score 452.6; DB 2 Pred. No. 1.7e-134 0; Mismatches

22.6%; 63.0%;

Conservative

Similarity

Query Match Best Loc Matches 257

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This sequence encodes the opossum parathyroid hormone (PTH) receptor OK-O, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia.
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                                                         gcaatacaggaaactggccaaatcgacactggtcctggtcctagtctttggagtgcatta 1216
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91US-0681702.
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PTH-related
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06-JUN-1995;
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A; 495 C; 522 G; 438 T; 0 other;

Sequence 1863 BP; 408

Thu Nov 16

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Total RNA was isolated from opossum kidney (OK) cells and used to prep. a cDNA ilbrary. The resultant phage libraries were used to transform E. coll contg. a larger helper plasmid p3. The cells were screened to isolate those expressing functionally intact OK cell parathyroid hormone/parathyroid hormone related protein (PTH/PTHFP) receptor proteins, performed according to Gearing et al., (EMBO J. 8 3676, 1989), by identifying colonies capable of binding a suitable radiolabelled ligand. The clone encodes a protein which may be used in a therapeutic compson. to inhibit activation of PTH or PTHFP and thus reduce the level of calcium in the blood. Cpds. Capable of competing with PTH or PTHFP for binding can be identified using fragments of the clone as probes. The sequence identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognessis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in See also Q29605-11.
ctgcaatggaggattcaggcagaggtgaagaagatgtggagtcggtggaatctccgt
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                          12:
  Length 1862;
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Score 451; DB 13;
Pred. No. 5.4e-134;
0; Mismatches 430;
22.5%;
63.0%;
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Query Match
Best Local Similarity
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                                            A cDNA clone (T15947), designated R15B ATCC 68571, codes for a rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHTP) receptor (R92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 CDNA library in pcDNA1 was used to transfect COS cells, and transfectants were selected for ability to bind labelled PTH. Recombinant receptor is produced in vector/host cell systems. The host cells can be used for diagnostic measurement of PTH serum levels. Transgenic chickens that overexpress the receptor in their oviduct lay eggs of higher calcium content.
       gcactgtgagctcttcttcaactcctttcagggtttctttgtgtctatcatctactgcta
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                                                                                           e.g. hypercalcaemia, hypo-calcaemia,
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73..1848
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91US-0681702
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                                                                                                                                                                                    (first entry)
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                                                                                                                                               T15947 standard;
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                                                                                                                                                                                    18-MAY-1996
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05-APR-1991;
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Score 445.2; DB 17; Length 2051; Pred. No. 4.2e-132;

22.2%; 62.9%;

Best Local Similarity

Query Match

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Pred. No. 4.2e-132;
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hypercalcaemia; rat;
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Best Local Similarity 62.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding parathyroid hormone receptor, DNA and antibodies or (differential) diagnosis of hypercalcaemia, and diagnosis
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                                                                                                          protein; calcium; antagonist;
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                                                                                   Rat bone PTH/PTHrP receptor clone, R15B.
                                                                                                                                                                     Location/Qualifiers
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/*tag= a
           Q29606 standard; cDNA; 2051 BP.
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Length 2051;

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0; Mismatches 425; 22.1%; Score 442; DB 13; 62.8%; Pred. No. 4.5e-131;

Conservative

Similarity

Best Local Sim. Matches 742;

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Query Match

gagaaggtaattgtttccctgaatgggatggactcatttgttggcccagaggaacagtgg 324

V08391

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 tgtctgccggaatgggaccacatcctgtgctggccgctggggggcaccaggtgaggtggtg 408
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1517 acttcaagcgcaaagcacgaagtgggagtagcagctacagct 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT;
                                                                                                                                                                    Human Parathyroid hormone receptor coding sequence
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Pred. No. 2.3e-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody to parathyroid hormone receptor therapeutic use
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28..1809
/*tag~ a
                                                                                                                                                                                                 hormone receptor; PTH ; hypercalcaemia; human;
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                                                                            BP
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Best Local Similarity 62.2%;
Matches 734; Conservative (
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95US-0471494
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Segre GV;
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P-PSDB; W73317.
                                                                        V08391 standard;
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PTH-related
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Q29607 standard; cDNA; 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A cDNA clone (T15948), designated HK-1, codes for human parathyroid hormone/parathyroid hormone-related protein (PTH/PTHIP) receptor (R92278). To obtain HK-1, a human kidney cDNA library was screened with a rate PTH/PTHIP cDNA clone (see T15946)ells. Recombinant receptor can be produced in vector/host cell systems. The host cells can be used for diagnostic measurement of PTH serum levels. Transgenic chickens that overexpress the receptor in their oviduct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                   Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgtttccctgaatgggatggactcatttgttggcccagaggaacagtgggaaaatatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding vertebrate parathyroid hormone receptor - useful diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 428.8; DB 17; Length 2010; Pred. No. 7.6e-127;
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pos:1472..1474:_aa:Ile
pos:1535..1537:_aa:Pro
pos:1757..1759:_aa:Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2010 BP; 468 A; 602 C; 567 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Potts JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 432;
                          Human kidney PTH/PTHrP receptor cDNA clone HK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Kronenberg HM,
                                                                                                                                             Location/Qualifiers
28..1810
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62.1%;
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91US-0681702.
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Pred. No. 8.6e-125;
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                   Human kidney PTH/PTHrP receptor clone
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/*tag= a
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                Porcine vasoactive intestinal peptide receptor; pig; lung tissue; amplification; primer; PCR; vasodilation; gastrointestinal tract;
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Pred. No. 1.6e-39;
0; Mismatches 248; Indels
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P-PSDB; R72506.
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Best Local Similarity
Matches 337; Conserv
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                                                                                                                                     19-APR-1995.
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                                                                    Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The DNA sequence encodes a secretin receptor of rat origin, contained in rat/mouse hybridoma NG108-15. The DNA sequence was obtd. from a cDNA library derived from NG108-15 cells. Expression in a suitable host allows prodn. of the receptor protein. The secretin receptor protein encoded by this gene may be used in basic research and in clinical tests, and is available in high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA coding for secretin receptor – is expressed in COS cells and produces a receptor protein for research and clinical use
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/note= "PCR primer binding site (3'-5')"
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277..1560
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P-PSDB; R30187.
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                  Gaps
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DB 13; Length 1794;
7.3%; Score 145.4; DB 13;
54.6%; Pred. No. 5.7e-36;
tive 0; Mismatches 286;
       al Similarity 54.6
365; Conservative
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Sequence 26, Sequence 26, Sequence 26, Sequence 24, Sequence 24, Sequence 24,

Sequence

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Sequence 1, Application US/08468011A; Sequence 1, Application US/08468011A; Sequence 1, 603804
Patent No. 6030804
Patent No. 6030804
PAPLICANT: Soppet, Daniel R
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Steven
APPLICANT: Ruben, Steven
APPLICANT: HVENTION: H-TDG74
TITLE OF INVENTION: H-TDG74
TITLE OF INVENTION: 128
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDITIONAL OF TOTAL OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 2003; DB 5; Query Match Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. 0; Mismatches 0; Matches 2003; Conservative
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COMPUTER: 1BM PG.2

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COMPUTER: WORD PERFECT 5.1

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA: 04.95

FILING DATE: 0.435

CLASSIFICATION: 0.435

CLASSIFICATION: 0.435

CLASSIFICATION: 0.435

THING DATE: 0.435

CLASSIFICATION: 1.700

TELERHONE: 3.0.194-1744

TELERHONE: 201-994-1744

TELERHONE: 201-994-1744

TELERHONE: 200-994-1744

TELERHONE: 200-994-1745

TERETONE CHARACTERISTICS: SECUENCE CHARACTERISTICS: SECUEN
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US-08-381-433A-3
US-08-110-286A-5
US-08-110-286A-5
US-08-111-14
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US-08-651-14
US-08-651-14
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US-08-651-14
US-08-452-2930-14
US-08-453-742-1
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US-08-453-742-24
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MOLECULE TYPE: CDNA
US-08-468-011A-1
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Sequence 34,
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Sequence 39,
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Sequence 2, Ap
Sequence 3, Ap
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Sequence 4, Ap
Sequence 4, Ap
Sequence 12, Ap
Sequence 13, A
Sequence 13, A
Sequence 13, A
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Sequence 11,
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copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
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                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07085
FILING DATE: 05-JUN-1995
CLASSIFICATION:
TITLE OF INVENTION: G-Protein Parathyroid
TITLE OF INVENTION: HITDG74
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2003;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                 ADDRESSEE: Carella, Byrne, Bain,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2003 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0%;
Matches 2003; Conservative (
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; LOCATION: 90..1712
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ZIP: 07068-1739
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                                                                        ggagcaacaaggaagatagtgggaggcagagagatgatattctaatggagaagccttcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Segre, Gino V.
APPLICANT: Segre, Gino V.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Juppner, Harald
APPLICANT: Octts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDULUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFICATION 0 435
PRIOR APPLICATION 0 435
FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00786/071002
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225 Franklin Street
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REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
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CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                          Length 1862;
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                                                                                                                                                                                                      Score 452.6; DB 1;
Pred. No. 1.4e-135;
0; Mismatches 429;
                                                                                                                                                                                                        22.6%;
63.0%;
(617) 542-5070
(617) 542-8906
                                                                                                                                                                                                        Query Match 22.6
Best Local Similarity 63.0
Matches 752; Conservative
                 TELEFAX: (617) 542-89C
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                    ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPLOGY: linear
US-07-864-475A-1
                                                                                    LENGTH: 1862
 TELEPHONE:
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                                               gcaatacaggaaactggccaaatcgacactggtcctggtcctagtcttggagtgcatta
                                                                                                                                                                                                                                                                                          APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00786/071003
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/468,249A FILING DATE: 06-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08468249A Patent No. 5886148 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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TOPOLOGY: 1
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; LOCATION:
US-08-468-249A-1
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 Length 1862;
                         Indels
Score 452.6; DB 3;
Pred. No. 1.4e-135;
0; Mismatches 429;
22.6%;
63.0%;
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Matches 752
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                                                   1402 GCACTATGAAATGCTCTTCAATTCATTCCAGGGATTTTTCGTTGCTTATATACTGTTT
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                                                                                                                                                                                                                                   APPLICANT: Segre, Gino V.
APPLICANT: Segre, Gino V.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 452.6; DB 1;
Pred. No. 1.4e-135;
0; Mismatches 429;
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

COMPUTER READALE FORM:

WEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: MOTOPERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00786/071002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/681,702
FILLING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 Sequence 2, Application US/07864475A Patent No. 5494806
                                                                                                                                                                                                                                                                                                                                                                          E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
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Matches 752; Conserv
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US-07-864-475A-2
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gcactgtgagctcttcttcaactcctttcagggtttctttgtgtctatcatctactgcta 1333
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                                                                      685 GGCTCCCTCACTGTGGCTGTGCTGATTCTGGGTTACTTTAGGAGGTTACATTGCACCCG 744
977 ggcacgagcaactctggctgatgcgaggtgctgggaacttagtgctggagacatcaagtg
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Kronenberg, Henry M.
Abou-Samra, Abdul-Badi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07864475A Patent No. 5494806 GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Juppner, Harald
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APPLICANT:
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                                                                                                                                         DNA
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                                                                                                                                         HORMONE RECEPTOR AND
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPACATORY
COMPUTER: DESCRIPTION PC-DOS/MS-DOS
COFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 452.6; DB 3;
Pred. No. 1.4e-135;
0; Mismatches 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00786/071003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                 APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HC
TITLE OF INVENTION: ENCODING SAME
                                                               Sequence 2, Application US/08468249A Patent No. 5886148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%;
63.0%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                          NUMBER OF SEQUENCES: 21
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STRANDEDNESS: single
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98..1853
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                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             02110-2804
                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY;
; LOCATION:
US-08-468-249A-2
                                                US-08-468-249A-2
                                                                                                                                                                                                                                                                STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
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COUNTRY:
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APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Encestina
TITLE OF INVENTION: PARATHYROLD HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 445.2; DB 1;
Pred. No. 3.7e-133;
0; Mismatches 423;
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/071002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/681,702
FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                   Richardson
                                                                                   225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%;
62.9%;
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(617) 542-8906
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.2
Best Local Similarity 62.9
Matches 744; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                             Massachusetts
                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                           COUNTRY: U.S.A.
                                                                                                 STREET: 225 Fr
CITY: Boston
STATE: Massach
                                                                                   ADDRESSEE:
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US-07-864-475A-3
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1038 1156 1098 1276 1275 1335 917 GCGTGGCGGTGACCTTCTTCCTGCTTACTTGCTACCAACTACTACTACTGGTGG tttatcaagcaccgatcttagcagctattgggctgaattttattctgtttctgaatacgg 797 CIGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGCGCCCTCACAGAGGAAGAGTTGC 745 cacaaaattccattgaggcaacttctgtggacaaatc----acaatatatcgggtgca 799 agattgctgttgtgatgtttatttacttcctggctacaaattattattggatcctggtgg ggggcttcatcttgataggctgggggtttccagcagcatttgttgcagcatgggctgtgg 1157 TCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCAACTTCATCATTTATCAACATCA ttagagttctagctaccaaaatctgggagaccaatgcagttgggcatgacacaaggaagc 1219 tcgtgttcgtgtgcctgcctcactcc---ttcactggggtcgggtgggagatccgcatgc actgtgagctcttcttcaactcctttcagggtttctttgtgtgtctatcatctactgctact gcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaatctctccgtgg Sequence 3. Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND TITLE OF INVENTION: ENCODING SAME NUMBER OF SEQUENCES: 21 1396 actggaaaaggacaccgccatgtggcagccgcagatgcggct 1437 

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1336 gcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaatctctccgtgg 1395 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
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                                                                           1276 actgtgagctcttcttcaactcctttcagggtttctttgtgtctatcatctactgctact
                                                 aaggtetetacetgcataateteatetttgtgggetttetttteggacaceaaataeetgt
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APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER EADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-BOS (Version 5.0)
SOFTWARE: WOTGPERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07864475A Patent No. 5494806 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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CORRESPONDENCE ADDRESS:
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ZIP: 02110-2804
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%; Score 445.2; DB 3; 62.9%; Pred. No. 3.7e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 00786/071003
                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                              APPLICATION NUMBER: US/08/468,249A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819 REFERENCE/DOCKET NUMBER: 007 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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Best Local Similarity
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; LOCATION:
US-08-468-249A-3
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APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY AGENT INFORMATION:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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REGISTRATION NUMBER: 3
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CITY: Boston
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US-08-468-249A-4
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Pred. No. 2.1e-128;
0; Mismatches 431;
                                                                           00786/071002
APPLICATION NUMBER: 07/681,702
                                                                       REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
            FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                      Ouery Match 21.5%;
Best Local Similarity 62.2%;
Matches 734; Conservative
                                                                                                                                                                                LENGTH: 2010
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-07-864-475A-4
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Patent No. 5886148
GENERAL INFORMATION
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND ITITE OF INVENTION: BROODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1407 acaccgccatgtggcagccgcagatgcggctcagtgctca 1446
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                                                            1230 tgcctgcctcactcct---tcactgggctcgggtgggagatccgcatgcactgtgagctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hsiung, Hansen M.
APPLICANT: Smith, Dennis P.
APPLICANT: Smith, Dennis P.
APPLICANT: Jang, Xing-Yue
TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                            acaccyccatytygcayccycayatycyyctca 1446
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Pred. No. 3.8e-40;
); Mismatches 248;
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COMPUTER: Macintosh Inci compatible
CERATING SYSTEM: System 7
SOFTWARE: Microsoft Word for Macintosh v.5.la
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08112817C
; Patent No. 5573928
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REGISTRATION NUMBER: 35,296
REFERENCE/DOCKET NUMBER: X-FELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3589
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ilarity 56.4%;
Conservative
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 337; Conservat
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COUNTRY: USA
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US-08-112-817C-1
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                                                                                                                                                       Length
                                                                                                                                                                                             Indels
                                                                                                                                                       Score 430.4; DB 3;
Pred. No. 2.1e-128;
0; Mismatches 431;
                                                                                                                                                   21.5%;
ilarity 62.2%;
Conservative
    single
                                                        CDS
28..1807
STRANDEDNESS: Sil
TOPOLOGY: linear
                                                                                                                                                                         Similarity
                                                        ; NAME/KEY:
; LOCATION:
US-08-468-249A-4
                                                                                                                                                                                           Matches 734;
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                                                                                                                                                                           Local
                                        FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1109 AAATGGTCTTTGAGCTCATCGTGGGATCTTTCCAGGGTTGTGTGGGGCCATCCTCTACT 1168
641 TGGGCTGTAAGGCAGCCGTGGTTTTATTCCAGTACTGTGTCATGGCCAACTTCTTCTGGC 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KITADA, Chleko
APPLICANT: ISHIBASHI, Yoshihiro
APPLICANT: HOSOYA, Masaki
APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HARMOTO, Yasunori
APPLICANT: HARMOTO, No. 585878710
APPLICANT: SHIMAMOTO, NO. 585878710
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
                              aatacctgtggggcttcatcttgataggctgggggtttccagcagcatttgttgcagcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,897A
FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/08811897A Patent No. 5858787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: OHTAKI, TETSUYA
T: MASUDA, Yasushi
T: KITADA, Chieko
T: ISHIBASHI, YOSHINIKO
T: HOSOYA, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO for Windo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ONDA, Haruo
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APPLICANT:
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1147 acacaaggaagcaatacaggaaactggccaaatcgacactggtcctggtcctagtctttg 1206
1028 AGTCCAGCATCTACTTACGG---CTGGCCCGCTCCACCTACTCCTACTTCG 1084
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Pred. No. 4.3e-28;
0; Mismatches 262;
                                                                                                  NAME: RESIGK, David S.
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPHONE: (617)523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1401 base pairs
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,986
FILING DATE: FEBRUATY 25, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08855213 Patent No. 5892004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.98;
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                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 1..1401
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-811-897A-32
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US-08-855-213-32
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1147 acacaaggaagcaatacaggaaactggccaaatcgacactggtcctggtcctagtctttg 1206
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                                                                                                                                                                         968 TCATCGGCATCATCATCATCCTTGTACAGAAGCTGCAGTCCCCAGACATGGGAGGCAACG 1027
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                                                                           908 CICIGIGGIGGIGAICAAAGGCCCCGIGGITGCCICIAIAAAGGTAACITIGIGIII
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APPLICANT: HABATA, Yugo
APPLICANT: HABATA, Yugo
APPLICANT: SHIRAMOTO, NO. 585978710
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
CORRESPONDENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                             1087 ttctgaatacggttagagttctagctaccaaaatctgggagaccaatgcagttgggcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,897A
FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 44168-DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/08811897A patent No. 5858787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: February 25, 1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHIBASHI, Yoshihiro
HOSOYA, Masaki
OGI, Kazuhiro
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TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: RESNICK, David S. REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)523-6440 INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OHTAKI, Tetsuya
MASUDA, Yasushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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APPLICANT:
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                                                                                             APPLICANT: ISHIBASH, VISALILIAN APPLICANT: ISHIBASH, Yoshihiro
APPLICANT: HOSOYA, Masaki
APPLICANT: GIL Kazulliro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABATA, Yugo
APPLICANT: HABATA, Yugo
APPLICANT: SHIAMOTO, No. 5892004io
TITLE OF INVENTION: PREPARING SAID PROTEIN, METHOD FOR
TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/85,213
FILNG DATE:
FILNG DATE: 25-FEB-1994
ATORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
REGISTENCE/DOCKET NUMBER: 34235
REGISTENCE/DOCKET NUMBER: 344168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118.8; DB 3;
Pred. No. 4.3e-28;
0; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELERAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1401 base pairs
TYPE: nucleic acid
STRANDENDESS: double
                                  OHTAKI, Tetsuya
MASUDA, Yasushi
KITADA, Chieko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.9%;
Best Local Similarity 53.7%;
Matches 321; Conservative (
                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: mat_peptide
; LOCATION: 1..1401
US-08-855-213-32
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
                    , Haruo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                  APPLICANT
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PREPARING SAID PROTEIN, AND USE THEREOF
                                            ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                    NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 (617)523-3400
(617)523-6440
                                                                         130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 1869 base pairs
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                       CITY: Boston
STATE: Massachusetts
                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
TITLE OF INVENTION:
               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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; LOCATION:
US-08-855-213-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                       COUNTRY:
                                                                            STREET:
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                                                                                                                                                                                    Length 1869;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABATA, Yuga
APPLICANT: HABATA, Yuga
APPLICANT: SHIAMOTO, NO. 5892004io
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR
                                                                                                                                                                                 Score 118.8; DB 3;
Pred. No. 5.2e~28;
0; Mismatches 262;
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MASUDA, Yasushi
KITADA, Chieko
ISHIBASHI, YOShihiro
HOSOYA, Masaki
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                                                                                                                                                                                 Ouery Match 5.9%;
Best Local Similarity 53.7%;
Matches 321; Conservative
            LENGTH: 1869 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS
                                                                                                      NAME/KEY: mat_peptide
LOCATION: 77..1477
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                                                                         MOLECULE TYPE: CDNA
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DIKE, BRONSTEIN, ROBERTS
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53.7%; Pred. No. 5.2e-zc,
...a 0; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,986
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S:
NAME: RESNICK, David S:
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Db 1104 AGTCCAGCATCTACTACGG----CTGGCCCGCTCCACCCTACTGCTCATCCCACTCTTCG 1160
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1207 gagtgcattacatcgtgttcgtgtgcctgcctcactccttcactgggctcgggtgggaga 1266 	1267 tccgcatgcactgtgagctcttctcaactcctttcagggtttctttgtgtctatcatct 1326	1212 AAAGACTTGTGTTTGAGCTTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCT 1271	1327 actgctactgcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaa 1384	1272 ACTGCTTCCTGAATGGGGAGGTACAGGCAGAGTAAGAGGAAATGGAGGAGAATTGGAGGAGAA 1329
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1207	1267	1212	1327	1272
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Search completed: November 15, 2000, 20:32:48 Job time: 3920 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	T.120953 DKF2p762	7 DKFZp7	5668 vf64c10.r	4986 1269	43796 DKFZp43	724325 HS_	0746 mv37a11.	3630 mh10g08.r	4442 6	'82 mi52e07.	592 mv28d07.	3394 137403	932	769 mv37c11	.57 uc81a02.	126	1119 UI-R-BJ	7170 mg54d06.	1036 EST237	3863 52606 MA	3470 AV5954	330	513 mm88a01.r	1526 BR_END	549 mg54d06.r	9889 HS_5080_A	1823 HS_556	2 HS_5569_	1000001		5534 HT-P-BT	377 EST66121	3313 EST250	1512	345828 Tetraod	9841 vw34g11.	174 EST34547	14173 E	1933 CIT-HSP-	396544 RPCI	93 vb79g06.	2602 ob10g0	77714 7B44E06 C	454
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% Query Match Length	0.5 450	5.1 35	9	2.3 54	1.6 25	1.1 36	.9 55	.8 65	.8 60	.6 40	.3 51	.6 41	.4 45	.4 55	.1 82	.1 54	.0 55	.9 70	.0 51	.8 33	.8 45	.7 37	.6 35	.5 46	.3 50	£.	2.84	5.2 865		0.0		.6	.6 35	5 65	.5 106	.3 51	.3 71	.2 70	.2 43	.1 55	24	.9 71	.8 24	.8
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ALIGNMENTS

This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the CDNA sequencing consortium of the German Genome Project. ö Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. No s1 sequence available.
This clone (DKF2p762E083) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. 1 (bases 1 to 450)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. BST (Koehrer, et al.)
Unpublished (1999)
Contact: Koehrer K 586 646 206 263 766 826 383 443 467 tegetttetgeagecagatateageataggaaageaagaattetgtgaaegeetetatgt 526 Gaps 83 sapiens cDNA clone /note="Vector: pSportl; Site\_1: NotI; Site\_2: SalI"
98 c 101 q 139 t agtaaaggagctggagtccctaataatgcaggatgacccacaaaattccattgaggcaac ; 0 Length 450; 1. 450
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/lab\_host="DH10B" Indels Am Klopferspitz 18a D-82152 Martinsried, Germany DKFZp762E083\_r1 762 (synonym: hmel2) Homo DKFZp762E083 5', mRNA sequence. Score 411; DB 14; Pred. No. 8.1e-110; 0; Mismatches 10; AL120953 AL120953.1 GI:5926954 20.5%; 97.7%; 450 bp Query Match 20.55 Best Local Similarity 97.7 Matches 417; Conservative ์ ๗ human. EST. source DEFINITION ORGANISM BASE COUNT ACCESSION VERSION REFERENCE AUTHORS TITLE JOURNAL 167 324 827 707 384 KEYWORDS FEATURES COMMENT SOURCE ORIGIN ŏ g ò q ò g δ P ò q ò Ω δy qq

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 667) Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3'); double-stranded cDNA was ligated to Eco RI adaptors [CATGGATTGGTACG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead."
                                                                                                                                            vf64c10.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:848562 5' similar to gb:X78936 M.musculus mRNA for parathyroid hormone (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:500714
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                                                                                                                               02-SEP-1997
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 9.3e-65;
0; Mismatches 188;
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      325 TTCTGTGGACAAATNACAATATATCGGGTGCA 356
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/lab_host="DH10B"
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Matches 383;
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                                                                                    RESULT
AA575668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 51 sequence available.
This clone (DKPZp7626243) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY: Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
Koehrer, K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 tttcatgctgagagctacaagcatctttgtcaaagacagagtagtccatgctcacatagg 706
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                                                                                                                                              mRNA EST 27-MAR-2000 (synonym: hmel2) Homo sapiens cDNA clone
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96 t 9 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
//organism="Homo sapiens"
//clone="DKE2p7626243"
//clone_lib="762 (synonym: hmel2)"
//tissue_type="melanoma (MeWo cell line)"
//dev_stage="adult"
/lab_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 ttctgtggacaaatcacaatatatcgggtgca 798
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82 c 79 q 9
                                                                                                                                          AL162097 356 bp mRNA
DKFZp762G243_r1 762 (synonym: hr
DKFZp762G243 5', mRNA sequence.
                                                                                                                                                                                                       AL162097
AL162097.1 GI:7330410
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Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 258)
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This is the 5' sequence of the clone insert
Clone Irom S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dKtz-haidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1160 atacaggaaactggccaaatcgacactggtcctggtcctagtctttggagtgcattacat 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgtgttcgtgtgcctgcctcactc...cttcactgggctcgggtgggagatccgcatgca 1276
                                                                                                                                                              800 gattgctgttgtgatgtttatttacttcctggctacaaattattattggatcctggtgga 859
                                                                                                                                                                                                                                      ALU43796 258 bp mRNA EST 29-FEB-2000 DKFZp434P0227_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P0227 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                gggcttcatcttgataggctgggggtttccagcagcatttgttgcagcatgggctgtggc
                                                                                                                                                                                                                                                                                                                                                                                   302 CCGGGTCCTTGCCACCACGAGGTGCGAACGCCGGCCGGTGTGACACGCGGCAGCA
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                                                                                                                                                                                   122 GGGCTTTACAGTCTTCGGCTGGGGTCTGCCTGCCATCTTCGTGGCTGTGTGGGTCAGTGT
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Pred. No. 2.2e-61;
0; Mismatches 174; Indels
                  145
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                139
30 embryos.
159 c 13
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Unpublished (1999)
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                                                                                      Query Match
12.3%;
Best Local Similarity 67.3%;
Matches 364; Conservative
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 and
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Contact: Smith TPL
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 PCR PRIMERS
PORMARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (base) I to 542)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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/lab_host-"bH10B"
/note="Vector: pCW SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                          1166
                                                                                                                                                                                                  1226
                                                    1106
                                                                                                                                                                                                                                                                      1227 gtgtgcctgcctcactcct--tcactgggctcgggtgggagatccgcatgcactgtgagc 1284
                                                                                                                                                                                                                                                                                                                                                tettetteaacteettteagggtttetttgtgtetateatetaetgetaetgeaatggag 1344
                                                                                                                                                                                                                                                                                                                                                                                                                       1345 aggitcaggcagaggtgaagaagatgiggagicggiggaatciccgiggaciggaaaa 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                           547
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128 ACCTTGGCCAACACTGGGTGCTGGGACCTGGGCACAAGAAGTGGATCATCCAG 187
                                                                                                                                                                307
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                                                    gcaccgatcttagcagctattgggctgaattttattctgtttctgaatacggttagagtt
                                                                                      188 GIGCCCATCCTGCCATCTGTGTGTCTCACTTCATCCTCTTTATCAACATCATCGGGTG
                                                                                                                            ctagetaceaaaatetgggagaeeaatgeagttgggeatgaeaaaggaageaataeagg
                                                                                                                                               488 AGGTGCAGGCAGAGATTAGGAAGTCTTGGAGCCGCTGGACACTGGCATTGGACTTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BEO14986 542 bp mRNA EST (
126918 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BEO14986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1405 ggacaccgccatgtggcagccgcagatgcggct 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 GTAAAGCACGAAGTGGAGTAGCAGCTACAGCT 580
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/organism-"Sus scrofa"
/db_xref-"taxon:9823"
/clone_lib-"MARC 1PIG"
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Plate: 57 row: L column: I
Seq primer: ATTTAGGTGACATATAG
Location/Qualifiers
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RESULT

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                                                                                             FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
Mahairas, G.C., Wailace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ724325 369 bp DNA GSS 14-JUL-1999
HS_2107_Al_BO6_MR CIT Approved Human Genomic Sperm Library D Homo
Sapiens genomic clone Plate=2107 Col=11 Row=C, DNA sequence.
sequenced by GBF (National Research Centre for Biotechnology Ltd.
Braunschweig/Germany) within the cDNA sequencing consortium of th
                                                              Berlin.
6, 14059
                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                pSport1; Site_1: NotI; Site_2: SalI"
76 g 48 t
                                                                                                                                                                                                                                                                                                                                                                 ;;
                           German Genome Project.
sl sequence also available.
This clone (DKFZp434P0227) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de.
                                                                                                                                                                                                                                                                                                                           Score 233; DB 14; Length 258;
Pred. No. 1.7e-57;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WA 98109, USA
                                                                                                                                     /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="Dkr2p434P0227"
/clone=lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Washington
401 Queen Anne Avenue North, Seattle,
Tel: (206) 516-3618
Fax: (206) 516-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center
                                                                                                                                                                                                                                                 /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ724325
AQ724325.1 GI:5483994
                                                                                                                                                                                                                                                                                                                             11.6%;
ilarity 99.6%;
Conservative (
                                                                                                                                                                                                                                                                 c 29
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                          Matches 244;
                                                                                                                                                                                                                                                                                                                                Query Match
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COMMENT
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SOURCE
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                                                                                                          FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 554)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 2107 row: C column: 11 Seg primer: M13 Reverse Class: BAC ends
                                                                                                                                                                                                                                                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1523
                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1345 aggttcaggcagaggtgaagaatgtggagtcggtggaatctctccgtggactggaaaa 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1524 ccaagatcgccagcagacagcctgacagccacatcactttacctggctatgtctggagta 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ATGTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGTGGAACCTCTCCGTGGACTGGAAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1465 ccagcagccagtcacagtggcgg-cagcacacgcatggtgcttatctctggcaaagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 108; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washu'HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                           1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 221.8; DB 108; Lengtl
Pred. No. 3.9e-54;
0; Mismatches 8; Indels
                                                                                                                                         High quality sequence stop: 369.
Location/Qualiflers
1. 369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2107 Col=11 Row=C"
                                                                                                                                                                                                                                                                                                                                                                                                                           ىد
                                                                                                                                                                                                                                                                                                                                                                                                                           81
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 11.1%;
al Similarity 96.3%;
237; Conservative
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: placenta; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 ctgttccatgccctccttatatttatgacttcaaccataaaggagttgctttccgacact 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGACCGCAATGGCAGCTGGGAGGTGGTTCCAGGGCACAACCGGACGTGGGCCAACTACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 cagactgccttcgctttctgcagccagatatcagcataggaaagcaagaattctgtgaac 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              goototatgtaatgtataccgttggotactccatctcttttggttccttggctgtggcta 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Gesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse placenta 4NbMP13.5 14.5" /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.5e-41;
); Mismatches 238;
                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                               MGI:267478
Putative full length read
vector to vector length is 831
Seq primer: ETPrimer
High quality sequence stop: 344.
Location/Qualifiers
                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:442142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J
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                                                                                     Waterston, R.
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                                                                                                                                                                                                                    Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 652)
                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1032 aagtggatttatcaagcaccgatcttagcagctattgggctgaattttattctgttctg 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgcatgcactgtgagctcttctaactcctttcagggtttctttgtgtctatcatctac 1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aatacggttagagttctagctaccaaaatctgggagaccaatgcagttgggcatgacaca 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AACATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACACC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AGGCAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTTGTGCCACTCTTCGGTGTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AAGTGGATCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCAACTTCATCCTCTTTATC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 CACTACACCGTCTTCATGGCCTTGCTGTACACCGAGGTCTCAGGGACACTGTGGCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 178; DB 2; Length 55
Pred. No. 3.6e-41;
0; Mismatches 125; Indels
                                                         MGI:403060
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1389 tccgtggactggaaaaggacaccgccatgtggca 1422
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                                                                                                                                                                /organism="Mus musculus"
Email: mouseest@watson.wustl.edu
                                                                                                High quality sequence stop: 288.
Location/Qualifiers
                                                                                                                                                                                    /strain-"C57BL/6J"
/db_xref-"taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 67.5%;
Matches 266; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_11"
/clone_lib="WIH_MGC_11"
/tissue_type="rhabdomyosarcoma"
/lab_host="MIH_MGC_11"
/flab_host="MIH_MGC_11"
/doct="Organ: muscle: Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tels: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Arayed by: The Lim.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM205 row: b column: 14
High quality sequence stop: 569.
Location/Qualifiers

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1. .608
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                                                                                                                       115 CAGGIGCCGCCTCCGCCGCCGCTGCTTGGTACGCTGCCTGCCGTGTGGCCGTGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                      BE294442 608 bp mRNA EST 20-JUL-2000 601176049F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531181
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 608)
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0; Mismatches 166;
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/db_xref="taxon:9606"
/clone="IMAGE:3531181"
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Best Local Similarity 61.6
Matches 371; Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA034782 406 bp mRNA EST 23-AUG-1996 mi52e07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:461172 5' similar to gb:X78936 M.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE);, mRNA sequence.
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gctgtggcacgagcaactctggctgatgcgaggtgctgggaacttagtgctggagacatc 1031
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Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
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house mouse.
Mus musculus
               AA242592.1
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This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:467172"
/clone=lib="Soares mouse embryo NbMEl3.5 14.5"
/sex-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 406;
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66.3%; Pred. No. 1.4e-39;
Live 0; Mismatches 131;
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                                                                                       1. .406
/organism≂"Mus musculus"
                                                        High quality sequence stop: 343.
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                             MGI:280988
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:402213
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                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.6e-37;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 165.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                              Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
GI:1873252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.3%;
Best Local Similarity 67.9%;
Matches 247; Conservative
                                                                                                                         (bases 1 to 515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1374
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);, mRNA sequence.

DEFINITION

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us-09-236-468a-1.rst

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/note="Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGTGGACGTGTATTTTTTTTTTTTTT-3'. CDNAS were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 456)
Marrad,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
Waterston,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                AI550932 456 bp mRNA EST 23-MAR-1999 vj65901.yl Knowles Solter mouse blastocyst B1 Mus musculus GDNA clone IMAGE:933936 5. similar to gb.x78936 м.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contract: Marshal-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                      739 atgacccacaaaattccattg---aggcaacttctgtggacaaatcacaatatcgggt 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                             251 AGCTGCGCGCCATTGCCCAGGCACCGCTGCCACCTGTCGCCGCCACCAACTACGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Knowles Solter mouse blastocyst B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 148.2; DB 11; Length
50.4%; Pred. No. 2e-32;
ve 0; Mismatches 168; Indels
                                                                                                                                                                           /tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:933936"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 60.4
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -40RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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VERSION
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COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                           AI550932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
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                                           g
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                                                                                                                             qq
                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 416)
Shahenkuug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
Tel: 402 762 4366
Fax: 402 762 4360
                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AGCCGCTGGACACTGGCATTGGACTTCAAGCGTAAAGCACGACGACGAGTAGCAGCTAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 CCTCCCTCACCGTGGCTGTCCTCATTCTGGCCTACTTCAGGAGGCTGCACTGCACACGCA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 agcaagaattctgtgaacgcctctatgtaatgtataccgttggctactccatcttttg 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagacagagtagtccatgctcacataggagtaaaggagctggagtccctaataatgcagg 738
                                                                                                                                                                                                10-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                           pig.
Sus scrofa
Sus scrofa
Mammalia; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                             BE232394 416 bp mRNA EST 1
137403 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 151.6; DB 34;
62.6%; Pred. No. 1.9e-33;
tive 0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 72 row: B column: 21
Seq primer: ATTTAGGGGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity 62.69
Matches 254; Conservative
                                                                                                                                                                                                                                           BE232394
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                                           1434 ggct 1437
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                                                                                                                                                    RESULT 1
BE232394
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                                                                                                                                                                                                                                                                                                                                                                                                        62
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Marthin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moors,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mv37cl1.rl GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA clone IMAGE:657236 5' similar to gb:x68596 PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE (HUMAN); gb:x78936 M.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                               618
                                                                                               135
                                                                                                                              678
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                                                                                                                             aagacagagtagtccatgctcacataggagtaaaggagctggagtccctaataatgcagg
                                                                                                                                                                                                                        196 AGGACGCTGTGCTCTGGCTTCACGCTGGATGAGGCCCGAGCGCCTCACGGAGGAAG
                                                                                                                                                                                                                                                                                        256 AGTIGCATATCATCGCGCAGGTGCCGCCTCCGCCCGCCGCTGCCGCTTGGCTACGCTG
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                  gttccttggctgtggctattctcatcattggttacttcagacgattgcattgcactagga
                                                                                                                                                                                                                                                          atgacccacaaaattccattgaggcaact----tctgtggacaaatcacaatatacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHML Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHML Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: -28m13 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism¬"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE WALS AND THE TOTAL MOIS AND THE TOTAL SEQ PLIMER: -28ml3 revl ET LO. High quality sequence stop: 22. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA240769.1 GI:1865143
                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 acctgtgggggttcatctt 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            );, mRNA sequence.
AA240769
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
AA240769
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA987157 827 bp mRNA EST 28-MAY-1998 uc81802.x1 Sugaron mouse kidney mkia Mus musculus cDNA clone IMAGE:1412010 3' similar to gb:x78936 M.musculus mRNA for parathyroid hormone/Parathyroid hormone (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1032 aagtggatttatcaagcaccgatcttagcagctattgggctgaattttattctgtttctg 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AAGTGGATCATCCAGGTGCCCATCCTGGCATCTGTTGTGTGCTCAACTTCATCTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 CAGGCAGCAGTACCGGAAGCTGCTCATGTCCACGTTGGTGCCTGTGCCACTCTTCGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1210 tgcattacatcgtgttcgtgtgcctgcct--cactccttcactgggctcgggtgggagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaggaagcaatacaggaaactggccaaatcgacactggtcctggtcctagtct-tggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TCCACTACACCGTCTTCATGGCCTTGCGTACACCGAGGTCTCAGGGACACTGTGGCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgcatgcactgtgagctcttcttcaactcctttcaggg-tttctttgtgtgtctatcatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1327 actgctactgcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.
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                                                                                                                                                                                                                                                                                                                                               Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1387 tetecegtegaectegaaaaaggaecaecegecategegeegeagetgeget 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                             7.4%; Score 148.2; DB 2;
66.4%; Pred. No. 2.1e-32;
tive 0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:916078
Seq primer name ambiguous
High quality sequence stop: 500.
Location/Qualifiers
1.827
/organism="Mus.musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1174 ccaaatcgacactggtcctggtcctagtctttggagtgcattacatcgtgttcgtgtgcc 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1234 tgcctcactcc---ttcactgggctcgggtgggagatccgcatgcactgtgagctcttct 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 142.2; DB 7; Length 827; ilarity 65.6%; Pred. No. 1.4e-30; Conservative 0; Mismatches 128; Indels 5.
                                                                                                                                    /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1432010"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
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                                                                                                                                                                                                 /dev_stage="adult"
                                                                                                                                                                                                           /lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 254;
                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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